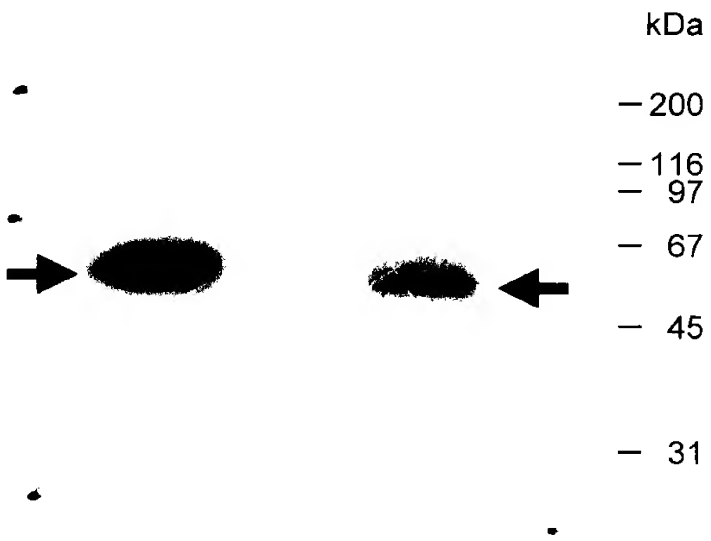


FIG.12

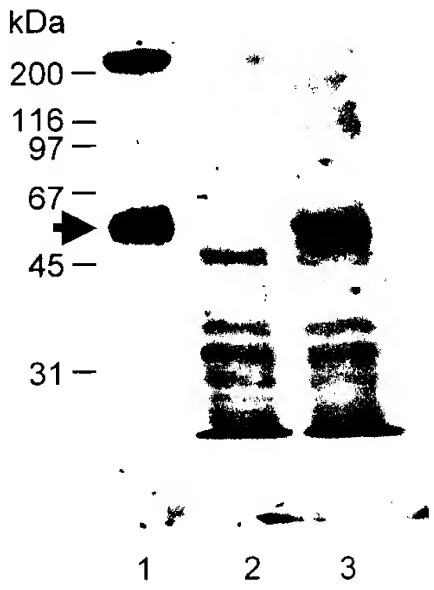


FIG.13A

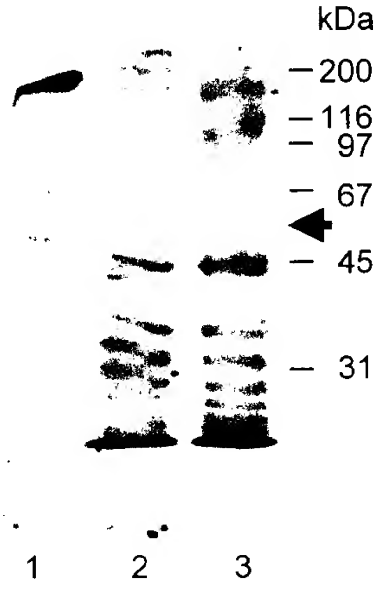


FIG.13B

FIG.14A

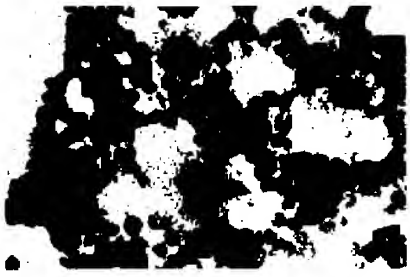


FIG.14B

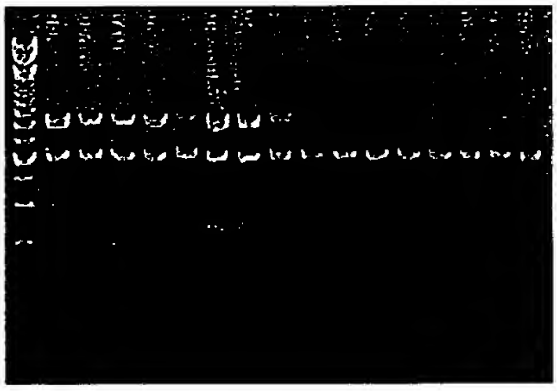


FIG.14C

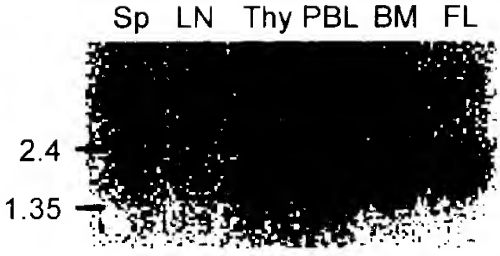


FIG.14D

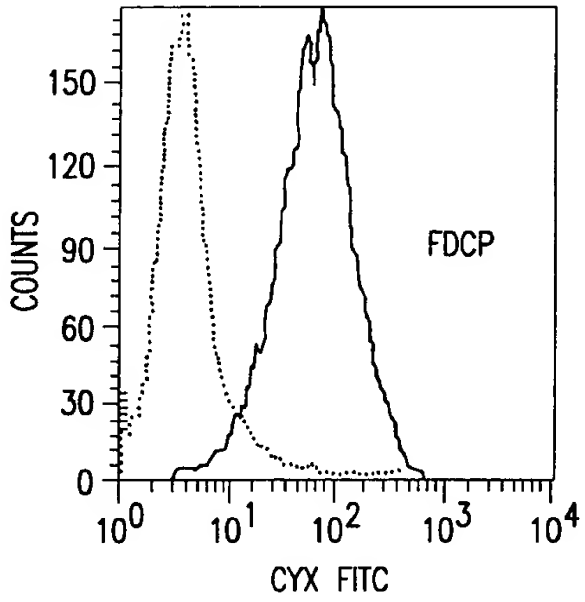


FIG.15A

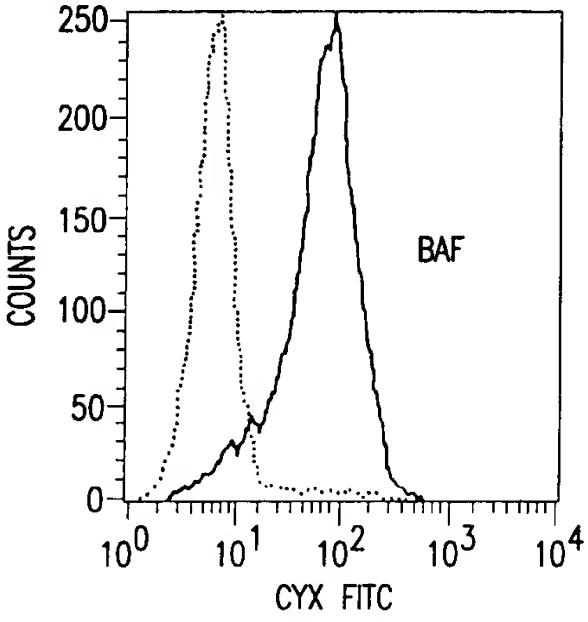


FIG.15B

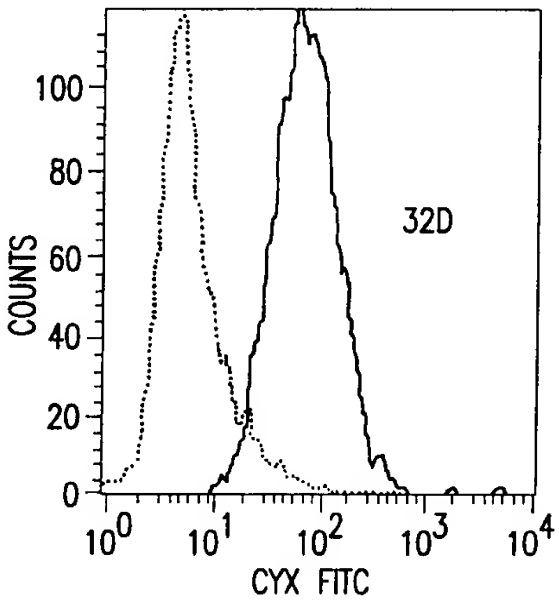


FIG.15C

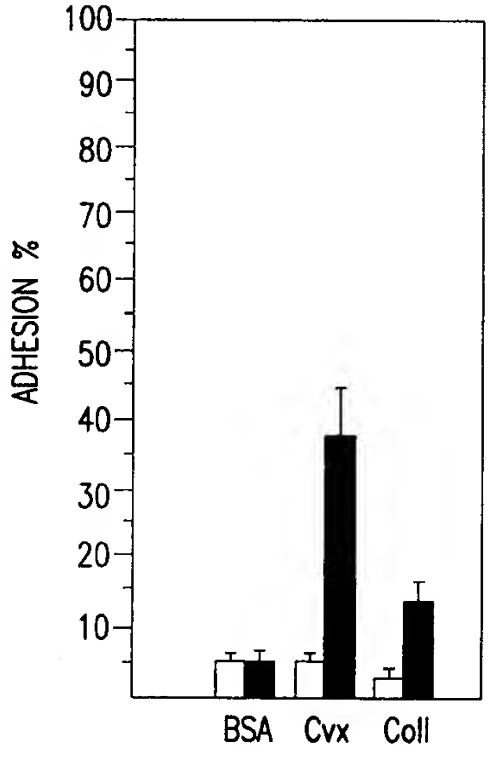


FIG.16A

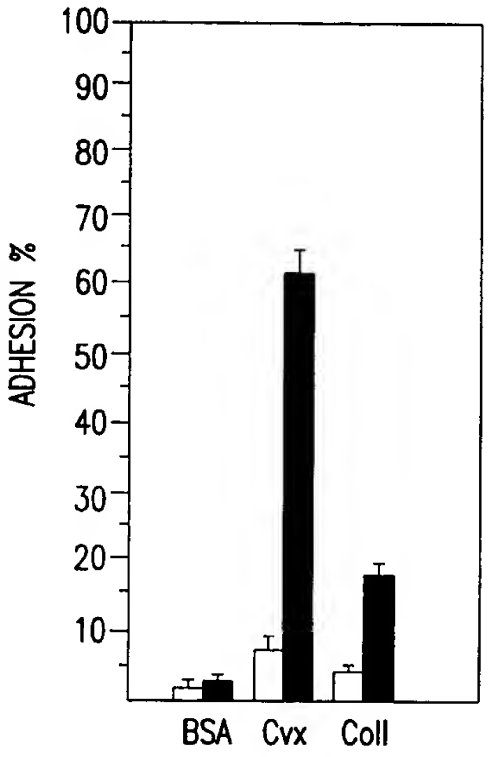


FIG.16B

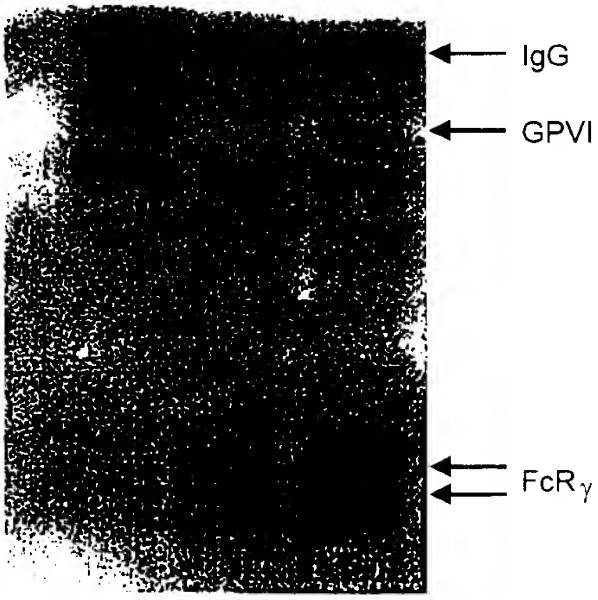


FIG. 17

Docket No.: 7853-178-999
Serial No.: 09/503,387
Inventor(s): BUSFIELD ET AL.
Title: "GLYCOPROTEIN VI AND USES THEREOF"

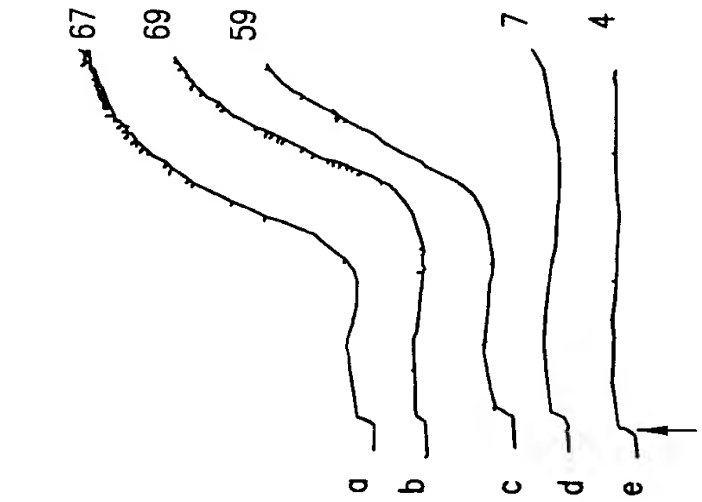


FIG.18B

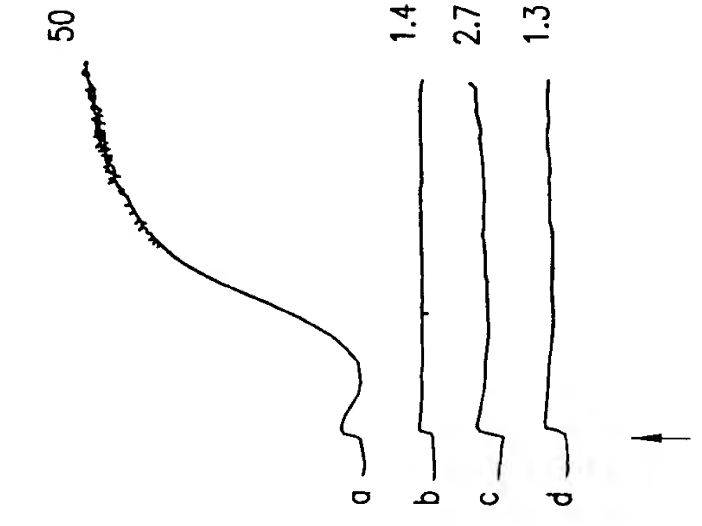


FIG.18A

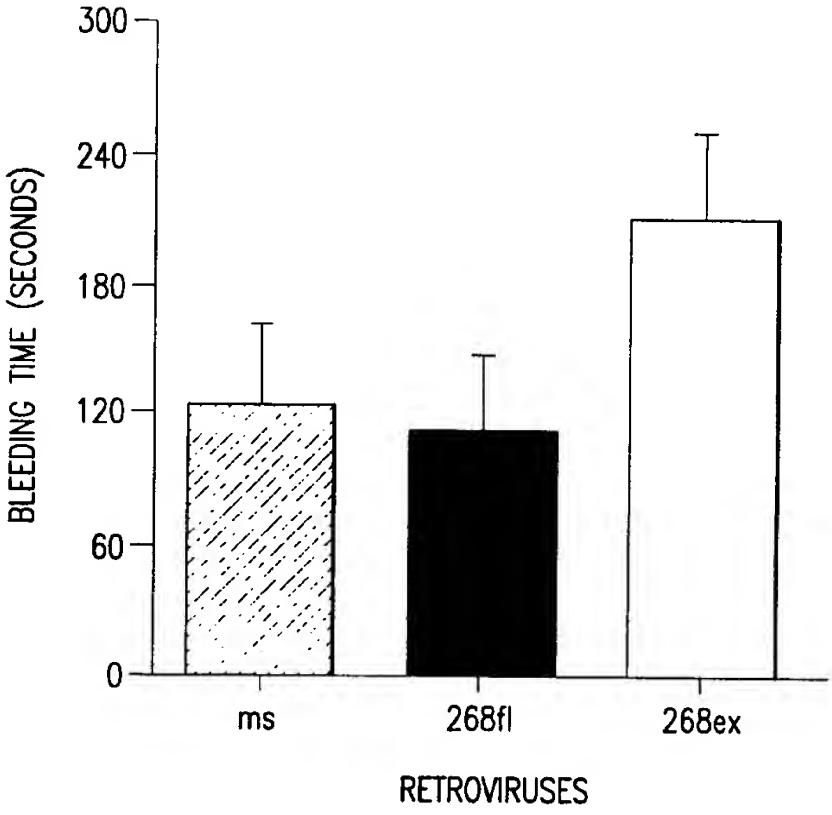


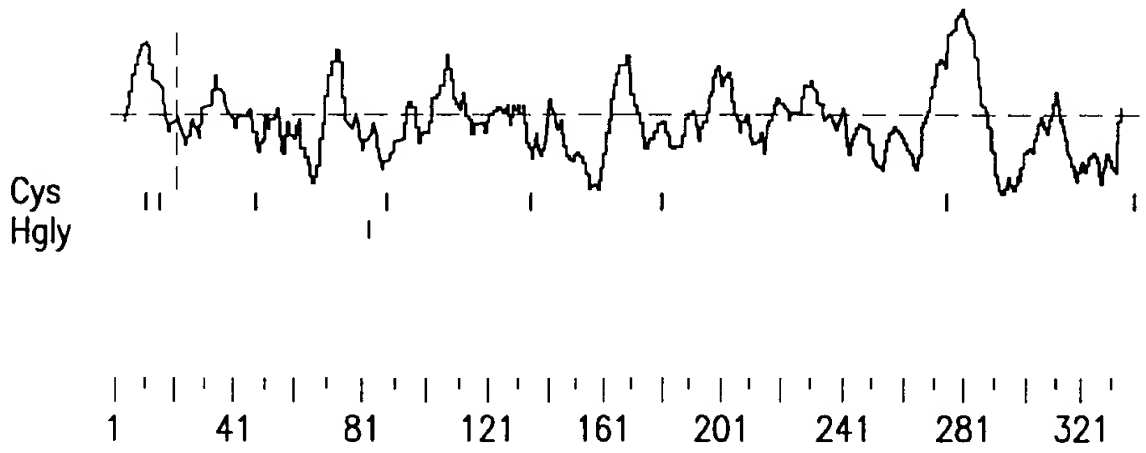
FIG.19

```
                                                  M   S   P   S   P   T   A   L   F   C   L    11
GGAGTCGACCCACGCGTCCGCAGGGCTGAGGAACC ATG TCT CCA TCC CCG ACC GCC CTC TTC TGT CTT    68

 G   L   C   L   G   R   V   P   A   Q   S   G   P   L   P   K   P   S   L   Q    31
GGG CTG TGT CTG GGG CGT GTG CCA GCG CAG AGT GGA CCG CTC CCC AAG CCC TCC CTC CAG   128

 A   L   P   S   S   L   V   P   L   E   K   P   V   T   L   R   C   Q   G   P    51
GCT CTG CCC AGC TCC CTG GTG CCC CTG GAG AAG CCA GTG ACC CTC CGG TGC CAG GGA CCT   188

 P   G   V   D   L   Y   R   L   E   K   L   S   S   S   R   Y   Q   D   Q   A    71
CCG GGC GTG GAC CTG TAC CGC CTG GAG AAG CTG AGT TCC AGC AGG TAC CAG GAT CAG GCA   248

 V   L   F   I   P   A   M   K   R   S   L   A   G   R   Y   R   C   S   Y   Q    91
GTC CTC TTC ATC CCG GCC ATG AAG AGA AGT CTG GCT GGA CGC TAC CGC TGC TCC TAC CAG   308

 N   G   S   L   W   S   L   P   S   D   Q   L   E   L   V   A   T   G   V   F   111
AAC GGA AGC CTC TGG TCC CTG CCC AGC GAC CAG CTG GAG CTC GTT GCC ACG GGA GTT TTT   368

 A   K   P   S   L   S   A   Q   P   G   P   A   V   S   S   G   G   D   V   T   131
GCC AAA CCC TCG CTC TCA GCC CAG CCC GGC CCG GCG GTG TCG TCA GGA GGG GAC GTA ACC   428

 L   Q   C   Q   T   R   Y   G   F   D   Q   F   A   L   Y   K   E   G   D   P   151
CTA CAG TGT CAG ACT CGG TAT GGC TTT GAC CAA TTT GCT CTG TAC AAG GAA GGG GAC CCT   488

 A   P   Y   K   N   P   E   R   W   Y   R   A   S   F   P   I   I   T   V   T   171
GCG CCC TAC AAG AAT CCC GAG AGA TGG TAC CGG GCT AGT TTC CCC ATC ATC ACG GTG ACC   548

 A   A   H   S   G   T   Y   R   C   Y   S   F   S   S   R   D   P   Y   L   W   191
GCC GCC CAC AGC GGA ACC TAC CGA TGC TAC AGC TTC TCC AGC AGG GAC CCA TAC CTG TGG   608

 S   A   P   S   D   P   L   E   L   V   V   T   G   T   S   V   T   P   S   R   211
TCG GCC CCC AGC GAC CCC CTG GAG CTT GTG GTC ACA GGA ACC TCT GTG ACC CCC AGC CGG   668

 L   P   T   E   P   P   S   S   V   A   E   F   S   E   A   T   A   E   L   T   231
TTA CCA ACA GAA CCA CCT TCC TCG GTA GCA GAA TTC TCA GAA GCC ACC GCT GAA CTG ACC   728

 V   S   F   T   N   K   V   F   T   T   E   T   S   R   S   I   T   T   S   P   251
GTC TCA TTC ACA AAC AAA GTC TTC ACA ACT GAG ACT TCT AGG AGT ATC ACC ACC AGT CCA   788

 K   E   S   D   S   P   A   G   P   A   R   Q   Y   Y   T   K   G   N   L   V   271
AAG GAG TCA GAC TCT CCA GCT GGT CCT GCC CGC CAG TAC TAC ACC AAG GGC AAC CTG GTC   848

 R   I   C   L   G   A   V   I   L   I   I   L   A   G   F   L   A   E   D   W   291
CGG ATA TGC CTC GGG GCT GTG ATC CTA ATA ATC CTG GCG GGG TTT CTG GCA GAG GAC TGG   908

 H   S   R   R   K   R   L   R   H   R   G   R   A   V   Q   R   P   L   P   P   311
CAC AGC CGG AGG AAG CGC CTG CGG CAC AGG GGC AGG GCT GTG CAG AGG CCG CTT CCG CCC   968
```

FIG.1A

```
 L   P   P   L   P   Q   T   R   K   S   H   G   G   Q   D   G   G   R   Q   D   331
CTG CCG CCC CTC CCG CAG ACC CGG AAA TCA CAC GGG GGT CAG GAT GGA GGC CGA CAG GAT 1028

 V   H   S   R   G   L   C   S   *                                               340
GTT CAC AGC CGC GGG TTA TGT TCA TGA                                             1055

CCGCTGAACCCCAGGCACGGTCGTATCCAAGGGAGGGATCATGGCATGGGAGGCGACTCAAAGACTGGCGTGTGTGGAG 1134

CGTGGAAGCAGGAGGGCAGAGGCTACAGCTGTGGAAACGAGGCCATGCTGCCTCCTCCTGGTGTTCCATCAGGGAGCCG 1213

TTCGGCCAGTGTCTGTCTGTCTGTCTGCCTCTCTGTCTGAGGGCACCCTCCATTTGGGATGGAAGGAATCTGTGGAGAC 1292

CCCATCCTCCTCCCTGCACACTGTGGATGACATGGTACCCTGGCTGGACCACATACTGGCCTCTTTCTTCAACCTCTCT 1371

AATATGGGCTCCAGACGGATCTCTAAGGTTCCCAGCTCTCAGGGTTGACTCTGTTCCATCCTCTGTGCAAAATCCTCCT 1450

GTGCTTCCCTTTGGCCCTCTGTGCTCTTGTCTGGTTTTCCCCAGAAACTCTCACCCTCACTCCATCTCCCACTGCGGTC 1529

TAACAAATCTCCTTTCGTCTCTCAGAACGGGTCTTGCAGGCAGTTTGGGTATGTCATTCATTTTCCTTAGTGTAAAACT 1608

AGCACGTTGCCCGCTTCCCTTCACATTAGAAAACAAGATCAGCCTGTGCAACATGGTGAAACCTCATCTCTACCAACAA 1687

AACAAAAAAACACAAAAATTAGCCAGGTGTGGTGGTGCATCCCTATACTCCCAGCAACTCGGGGGGCTGAGGTGGGAGA 1766

ATGGCTTGAGCCTGGGAGGCAGAGGTTGCAGTGAGCTGAGATCACACCACTGCACTCTAGCTCGGGTGACGAAGCCTGA 1845

CCTTGTCTCAAAAAATACAGGGATGAATATGTCAATTACCCTGATTTGATCATAGCACGTTGTATACATGTACTGCAAT 1924

ATTGCTGTCCACCCCATAAATATGTACAATTATGTATACATTTTTAAAATCATAAAAATAAGATAATGAAAAAAAAAAA 2003

AAAAAAAAAAAAAAAGGGCGGGCCGCTAGACTAGTCTAGAGAACA                                   2047
```

FIG.1B



MSPSPTALFCLGLCLGRVPAQSGPLPKPSLQALPSSLVPLEKPVTLRCQGPPGVDLYRLE
KLSSSRYQDQAVLFIPAMKRSLAGRYRCSYQNGSLWSLPSDQLELVATGVFAKPSLSAQP
GPAVSSGGDVTLQCQTRYGFDQFALYKEGDPAPYKNPERWYRASFPIITVTAAHSGTYRC
YSFSSRDPYLWSAPSDPLELVVTGTSVTPSRLPTEPPSSVAEFSEATAELTVSFTNKVFT
TETSRSITTSPKESDSPAGPARQYYTKGNLVRICLGAVILIILAGFLAEDWHSRRKRLRH
RGRAVQRPLPPLPPLPQTRKSHGGQDGGRQDVHSRGLCS

FIG.2

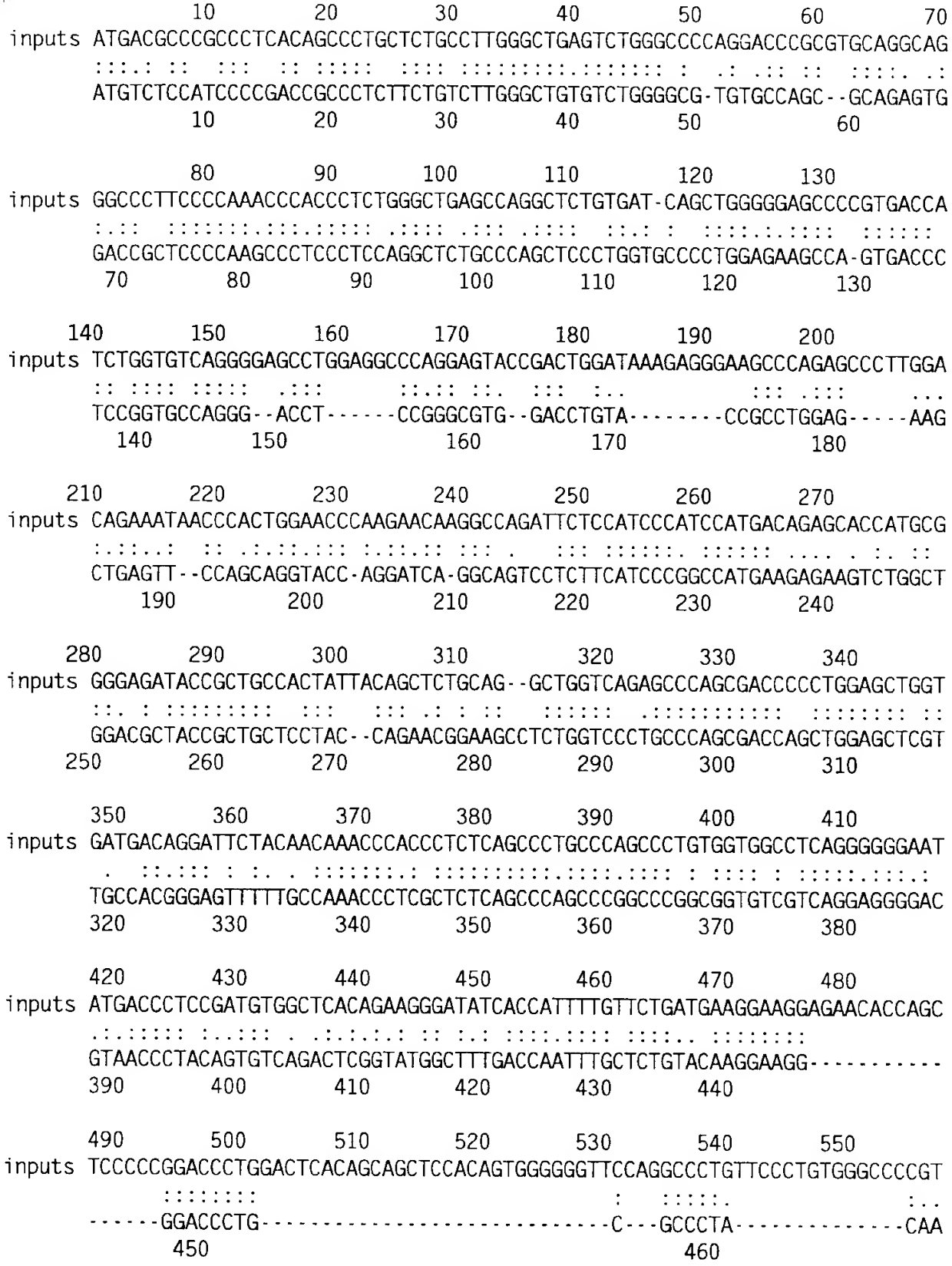


FIG.3A

```
          560        570        580        590        600        610        620
inputs    GAACCCCAGCCACAGGTGGAGGTTCACATGCTATTACTATTATATGAACACCCCCCAGGTGTGGTCCCAC
          ::: ::::..       :.:.::::.: :. :::: :     ::           :::::          ::
          GAATCCCGA------GAGATGGTAC-CGGGCTAGT----TT-----------CCCCAT---------CAT
             470             480        490                      500

          630        640        650        660        670        680        690
inputs    CCCAGTGACCCCCTGGAGATTCTGCCCTCAGGCGTGTCTAGGAAGCCCTCCCTCCTGACCCTGCAGGGCC
          : :.::::::: ::           ::::.:::
          CACGGTGACCGCC----------GCCCACAG-----------------------------------
              510                  520

          700        710        720        730        740        750        760
inputs    CTGTCCTGGCCCCTGGGCAGAGCCTGACCCTCCAGTGTGGCTCTGATGTCGGCTACGACAGATTTGTTCT
                           :.::::::.     ::..::              ::::::.:       ::::
          ----------------CGGAACCTA-----CCGATG--------------CTACAGC-------TTCT
                           530                              540                550

          770        780        790        800        810        820        830
inputs    GTATAAGGAGGGGGAACGTGACTTCCTCCAGCGCCCTGGCCAGCAGCCCCAGGCTGGGCTCTCCCAGGCC
                                                  :::::::
          ---------------------------------------CCAGCAG----------------------

          840        850        860        870        880        890        900
inputs    AACTTCACCCTGGGCCCTGTGAGCCCCTCCCACGGGGGCCAGTACAGGTGCTATGGTGCACACAACCTCT
                    ::.:::.                                                 .::::
          -----------GGACCCA-------------------------------------------------TACCT--
                     560

          910        920        930        940        950        960        970
inputs    CCTCCGAGTGGTCGGCCCCCAGCGACCCCCTGAACATCCTGATGGCAGGACAGATCTATGACACCGTCTC
                 :::::::::::::::::::::::::::.:          ::.          :.::
          -------GTGGTCGGCCCCCAGCGACCCCCTGGA----------GCT---------TGTG----------
                570        580        590                         600

          980        990       1000       1010       1020       1030       1040
inputs    CCTGTCAGCACAGCCGGGCCCCACAGTGGCCTCAGGAGAGAACGTGACCCTGCTGTGTCAGTCATGGTGG
             ::::        :.::  ::.:::::.::                  :::.::     :.::
          ---GTCA-------CAGGAACCTCTGTGACC---------------CCCAGC-----CGGT--------
                        610        620                         630

         1050       1060       1070       1080       1090       1100       1110
inputs    CAGTTTGACACTTTCCTTCTGACCAAAGAAGGGGCAGCCCATCCCCCACTGCGTCTGAGATCAATGTACG
                    :.::.:.:: :           ::  ::.:::                          .::
          -----------TACCAACAGAAC----------CA--CCTTCC---------------------------TCG
                     640                       650

         1120       1130       1140       1150       1160       1170       1180
inputs    GAGCTCATAAGTACCAGGCTGAATTCCCCATGAGTCCTGTGACCTCAGCCCACGCGGGGACCTACAGGTG
          :..                 ::.::::::: :         .:..::.:      ::: :.     ::.:  .
          GTA-------------GCAGAATTCTC---------AGAAGCCAC------CGCTGA-----ACTG--A
          660                      670                 680                  690
```

FIG.3B

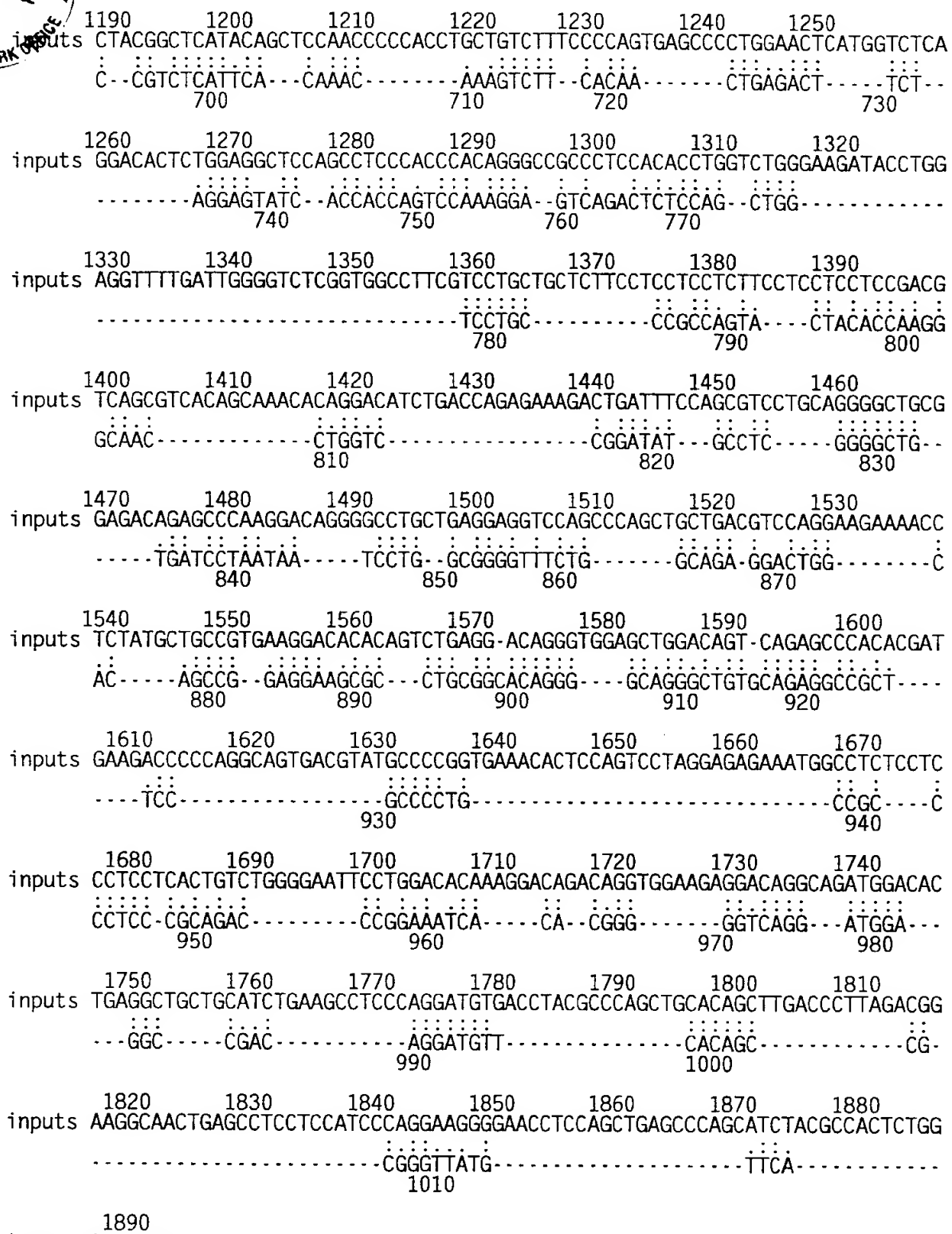


FIG.3C

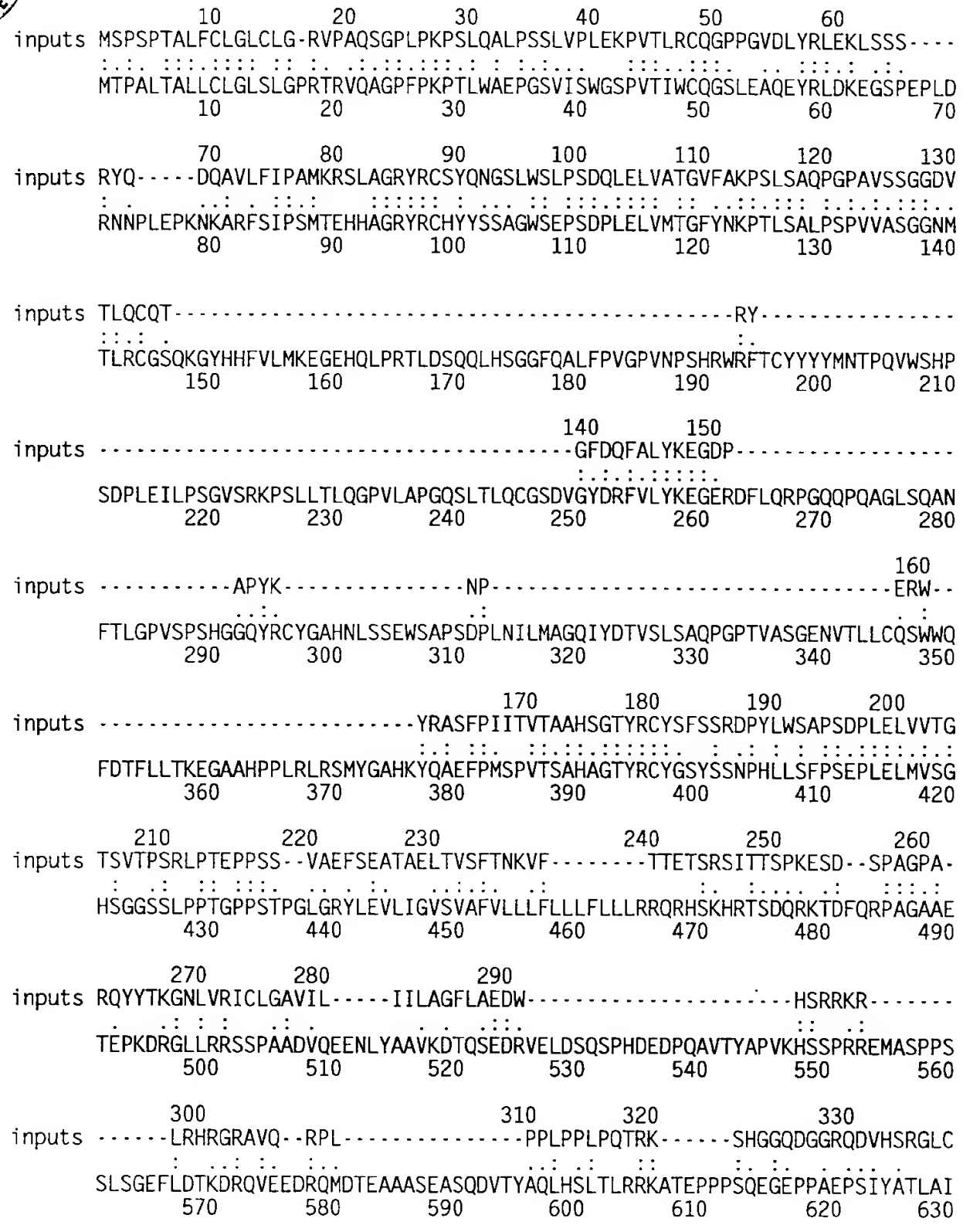


FIG.4

```
                *->GesvtLtCsvsgfgppgvsvtWyfkngk.lgpsllgysysrlesgek
                   + vtL+C+         + v  y +  k  ++         r++ +
hT268     41    EKPVTLRCQGP------PGVDLY-RLEKISSS--------RYQDQ--  70

                anlsegrfsissltLtissvekeDsGtYtCvv<-*
                           ++L i   +++ +G Y+C
hT268     71    ------------AVLFIPAMKRSLAGRYRCSY     90
```

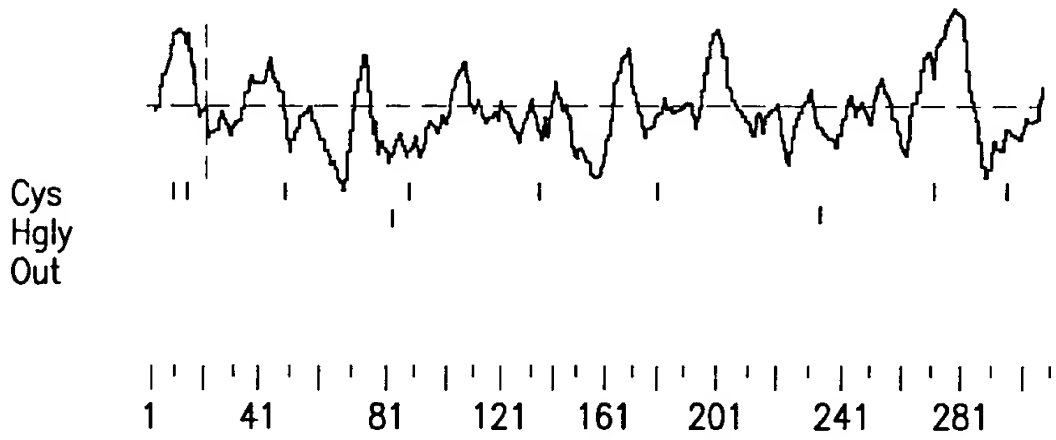
FIG.5A

```
                *->GesvtLtCsvsgfgppgvsvtWyfkngk.lgpsllgysysrlesgek
                  G++vtL+C+++    +  ++  y k+g++ +     y+++
hT268     127   GGDVTLQCQTR---YGFDQFALY-KEGDpAP-----YKNPERWYR--  162

                anlsegrfsissltLtissvekeDsGtYtCvv<-*
                          ++++i++v++  sGtY+C
hT268     163   ------------ASFPIITVTAAHSGTYRCYS     182
```

FIG.5B

```
                                                                  M   S   P   A      4
GAGTCGACCCACGCGTCCGCTTCCCTGCTTGGCCACATAGCTCAGGACTGGGTTGCAGAACC ATG TCT CCA GCC     74

 S   P   T   F   F   C   I   G   L   C   V   L   Q   V   I   Q   T   Q   S   G     24
TCA CCC ACT TTC TTC TGT ATT GGG CTG TGT GTA CTG CAA GTG ATC CAA ACA CAG AGT GGC    134

 P   L   P   K   P   S   L   Q   A   Q   P   S   S   L   V   P   L   G   Q   S     44
CCA CTC CCC AAG CCT TCC CTC CAG GCT CAG CCC AGT TCC CTG GTA CCC CTG GGT CAG TCA    194

 V   I   L   R   C   Q   G   P   P   D   V   D   L   Y   R   L   E   K   L   K     64
GTT ATT CTG AGG TGC CAG GGA CCT CCA GAT GTG GAT TTA TAT CGC CTG GAG AAA CTG AAA    254

 P   E   K   Y   E   D   Q   D   F   L   F   I   P   T   M   E   R   S   N   A     84
CCG GAG AAG TAT GAA GAT CAA GAC TTT CTC TTC ATT CCA ACC ATG GAA AGA AGT AAT GCT    314

 G   R   Y   R   C   S   Y   Q   N   G   S   H   W   S   L   P   S   D   Q   L    104
GGA CGG TAT CGA TGC TCT TAT CAG AAT GGG AGT CAC TGG TCT CTC CCA AGT GAC CAG CTT    374

 E   L   I   A   T   G   V   Y   A   K   P   S   L   S   A   H   P   S   S   A    124
GAG CTA ATT GCT ACA GGT GTG TAT GCT AAA CCC TCA CTC TCA GCT CAT CCC AGC TCA GCA    434

 V   P   Q   G   R   D   V   T   L   K   C   Q   S   P   Y   S   F   D   E   F    144
GTC CCT CAA GGC AGG GAT GTG ACT CTG AAG TGC CAG AGC CCA TAC AGT TTT GAT GAA TTC    494

 V   L   Y   K   E   G   D   T   G   P   Y   K   R   P   E   K   W   Y   R   A    164
GTT CTA TAC AAA GAA GGG GAT ACT GGG CCT TAT AAG AGA CCT GAG AAA TGG TAC CGG GCC    554

 N   F   P   I   I   T   V   T   A   A   H   S   G   T   Y   R   C   Y   S   F    184
AAT TTC CCC ATC ATC ACA GTG ACT GCT GCT CAC AGT GGG ACG TAC CGG TGT TAC AGC TTC    614

 S   S   S   S   P   Y   L   W   S   A   P   S   D   P   L   V   L   V   V   T    204
TCC AGC TCA TCT CCA TAC CTG TGG TCA GCC CCG AGT GAC CCT CTA GTG CTT GTG GTT ACT    674

 G   L   S   A   T   P   S   Q   V   P   T   E   E   S   F   P   V   T   E   S    224
GGA CTC TCT GCC ACT CCC AGC CAG GTA CCC ACG GAA GAA TCA TTT CCT GTG ACA GAA TCC    734

 S   R   R   P   S   I   L   P   T   N   K   I   S   T   T   E   K   P   M   N    244
TCC AGG AGA CCT TCC ATC TTA CCC ACA AAC AAA ATA TCT ACA ACT GAA AAG CCT ATG AAT    794

 I   T   A   S   P   E   G   L   S   P   P   I   G   F   A   H   Q   H   Y   A    264
ATC ACT GCC TCT CCA GAG GGG CTG AGC CCT CCA ATT GGT TTT GCT CAT CAG CAC TAT GCC    854

 K   G   N   L   V   R   I   C   L   G   A   T   I   I   I   I   L   L   G   L    284
AAG GGG AAT CTG GTC CGG ATA TGC CTT GGT GCC ACG ATT ATA ATA ATT TTG TTG GGG CTT    914

 L   A   E   D   W   H   S   R   K   K   C   L   Q   H   R   M   R   A   L   Q    304
CTA GCA GAG GAT TGG CAC AGT CGG AAG AAA TGC CTG CAA CAC AGG ATG AGA GCT TTG CAA    974

 R   P   L   P   P   L   P   L   A   *                                           314
AGG CCA CTA CCA CCC CTC CCA CTG GCC TAG                                         1004

AAATAACTTGGCTTTCAGCAGAGGGATTGACCAGACATCCATGCACAACCATGGACATCACCACTAGAGCCACAGACAT 1083
GGACATACTCAAGAGTGGGGAGGTTATATAAAAAAATGAGTGTGGAGAATAAATGCAGAGCCAACAAGGTGAAAAAAAA 1162
A                                                                               1163
```

FIG.6



MSPASPTFFCIGLCVLQVIQTQSGPLPKPSLQAQPSSLVPLGQSVILRCQGPPDVDLYRL
EKLKPEKYEDQDFLFIPTMERSNAGRYRCSYQNGSHWSLPSDQLELIATGVYAKPSLSAH
PSSAVPQGRDVTLKCQSPYSFDEFVLYKEGDTGPYKRPEKWYRANFPIITVTAAHSGTYR
CYSFSSSSPYLWSAPSDPLVLVVTGLSATPSQVPTEESFPVTESSRRPSILPTNKISTTE
KPMNITASPEGLSPPIGFAHQHYAKGNLVRICLGATIIIILLGLLAEDWHSRKKCLQHRM
RALQRPLPPLPLA

FIG.7

```
                10        20        30        40        50        60        70
inputs ATGACGCCCGCCCTCACAGCCCTGCTCTGCCTTGGGCTGAGTCTGGGCCCCAGGACCCGCGTGCAGGCAG
       ::::: :: ::: :::: ::    .::  :::   :::..:
       ATGTCTCCAGCC-TCAC--CC----ACTTTCTT---CTGTAT-------------------------
                10              20          30

                80        90       100       110       120       130       140
inputs GGCCCTTCCCCAAACCCACCCTCTGGGCTGAGCCAGGCTCTGTGATCAGCTGGGGGAGCCCCGTGACCAT
                          :::::::          ::::..:.::
       ----------------------TGGGCTG---------TGTGTACTGC-----------------
                                           40

               150       160       170       180       190       200       210
inputs CTGGTGTCAGGGGAGCCTGGAGGCCCAGGAGTACCGACTGGATAAAGAGGGAAGCCCAGAGCCCTTGGAC
                                 :.:.:..::                ::.: :::::    :::
       --------------------------AAGTGATCC---------------AAACACAGAG----TGG--
                                 50                       60            70

               220       230       240       250       260       270       280
inputs AGAAATAACCCACTGGAACCCAAGAACAAGGCCAGATTCTCCATCCCATCCATGACAGAGCACCATGCGG
                :::::    :::     ::::          ::.:::: :::: :
       --------CCCACT----CCC-----CAAG---------CCTTCCC-TCCAGG--------------
                         80                         90

               290       300       310       320       330       340       350
inputs GGAGATACCGCTGCCACTATTACAGCTCTGCAGGCTGGTCAGAGCCCAGCGACCCCCTGGAGCTGGTGAT
                : :.:::                        :::. :::.: :. ::::::: :.:
       --------CTCAGCC-----------------------CAGTTCCCTG-GTACCCCTGGGTCAG-----
                100                          110       120

               360       370       380       390       400       410       420
inputs GACAGGATTCTACAACAAACCCACCCTCTCAGCCCTGCCCAGCCCTGTGGTGGCCTCAGGGGGGAATATG
                .:::  :: :.:                                ::.::::  :  :::::.
       -TCAG--TTATTC-------------------------------TGAGGTG-C--CAGGGA--------
       130                                        140       150

               430       440       450       460       470       480
inputs ACCCTCC-GATGTGGCTCACAGAAGGGATATCACCATTTTGTTCTGATGAAGGAAGGAGAACACCAGCTC
                :::::  :::::::         :   ::::::.::.  . ..:::::..
       --CCTCCAGATGTGG--------ATTTATATCGCCTGGAGAAACTGAAA-------------------
                160               170       180       190

           490       500       510       520       530       540       550
inputs CCCCGGACCCTGGACTCACAGCAGCTCCACAGTGGGGGGTTCCAGGCCCTGTTCCCTGTGGGCCCCGTGA
                :::::     ::                  :::. :..:.:: ::.:    ::: ::        :.:
       --CCGGA-----GA----------------AGTATGAAGATCAAGAC---TTTCTCTT-------CATT-
                                      200       210       220
```

FIG. 8A

```
          560        570        580        590        600        610        620
inputs ACCCCAGCCACAGGTGGAGGTTCACATGCTATTACTATTATATGAACACCCCCCAGGTGTGGTCCCACCC
          :::.::: .:...::.::.    :::::              :.::        ::::.:
       ---CCAACCATGGAAAGAAGTA---ATGCT------------GGAC--------GGTAT----------
          230        240        250                          260

          630        640        650        660        670        680        690
inputs CAGTGACCCCCTGGAGATTCTGCCCTCAGGCGTGTCTAGGAAGCCCTCCCTCCTGACCCTGCAGGGCCCT
          :..::   : :: .          ::::.      ..::.:: :                .:.:: : ::
       CGATG---CTCTTA----------TCAGA------ATGGGAGTC--------------ACTGGTCTCT
                  270                      280                      290

          700        710        720        730        740        750        760
inputs GTCCTGGCCCCTGGGCAGAGCCTGACCCTCCAGTGTGGCTCTGATGTCGGCTACGACAGATTTGTTCTGT
                  :::..:        :::::  : .:.:     ::.::    :::::
       --------CCCAAG--------TGACCAGCTTGAG-----CTAATT---GCTAC--------------
             300                310              320

          770        780        790        800        810        820        830
inputs ATAAGGAGGGGGAACGTGACTTCCTCCAGCGCCCTGGCCAGCAGCCCCAGGCTGGGCTCTCCCAGGCCAA
          :::.: : ...: ..::  ::::                                .:::::
       ---AGGTGTGTATGCTAAAC--CCTC----------------------------ACTCTC---------
             330        340                                    350

          840        850        860        870        880        890        900
inputs CTTCACCCTGGGCCCTGTGAGCCCCTCCCACGGGGGCCAGTACAGGTGCTATGGTGCACACAACCTCTCC
                           ::: : :::::                  :::
       ------------------AGCTCATCCCA----------------GCT------------------
                              360

          910        920        930        940        950        960        970
inputs TCCGAGTGGTCGGCCCCCAGCGACCCCCTGAACATCCTGATGGCAGGACAGATCTATGACACCGTCTCCC
                        :::::.. :::       ::   :.:::::::   :::  .::::.: :.
       ----------------CAGCAGTCCC-------TC---AAGGCAGG---GAT--GTGACTCTGA-----
                        370                380          390          400

          980        990        1000       1010       1020       1030       1040
inputs TGTCAGCACAGCCGGGCCCCACAGTGGCCTCAGGAGAGAACGTGACCCTGCTGTGTCAGTCATGGTGGCA
          .::       :::.:. :::: :                                  :::: .::.::.
       AGT-------GCCAGAGCCCATA--------------------------------CAGTTTTGATGA--
                     410                                        420

          1050       1060       1070       1080       1090       1100       1110
inputs GTTTGACACTTTCCTTCTGACCAAAGAAGGGGCAGCCCATCCCCCACTGCGTCTGAGATCAATGTACGGA
                  .::: :::::. ::::::::::      ::     :::: : :: : :  :..:. : ::
       ---------ATTCGTTCTATACAAAGAAGGGG------AT-----ACTGGGCCTTATA--AGAGACCTGA
                 430        440        450                460        470
```

FIG.8B

FIG.8C

```
    1750       1760       1770       1780       1790       1800       1810
inputs GCTGCTGCATCTGAAGCCTCCCAGGATGTGACCTACGCCCAGCTGCACAGCTTGACCCTTAGACGGAAGG
       ::  ::::::.:.          ::::::::.::                    :::: .:          .::::
       GC--CTGCAACA---------CAGGATGAGA-----------------GCTTTGC---------AAAGG
             890                900                          910

    1820       1830       1840       1850       1860       1870       1880
inputs CAACTGAGCCTCCTCCATCCCAGGAAGGGGAACCTCCAGCTGAGCCCAGCATCTACGCCACTCTGGCCAT
       : :::.     ::.::                 :::::                          :.:::::::
       CCACTA-----CCACC---------------CCTCC----------------------CACTGGCC--
         920                           930

    1890
inputs CCAC
```

FIG. 8D

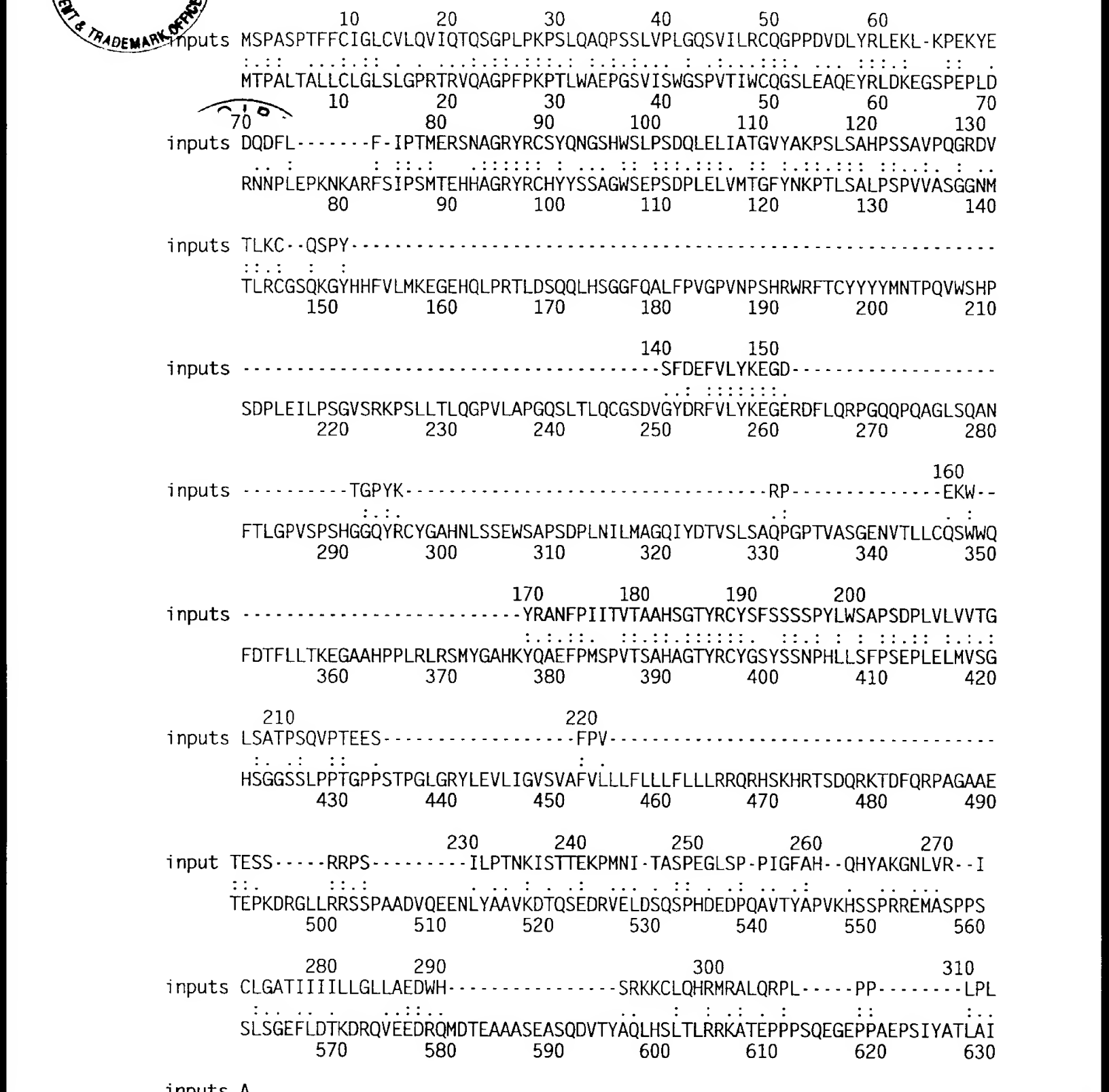


FIG. 9

```
                *->GesvtLtCsvsgfgppgvsvtWyfkngk.lgpsllgysysrlesgek
                   G+sv L+C+        ++v  y +  k ++        +++e +
mT268     42    GQSVILRCQGP------PDVDLY-RLEKlKP--------EKYEDQ-- 71

                   anlsegrfsissltLtissvekeDsGtYtCvv<-*
                                L i + e++++G Y+C
mT268     72    ------------DFLFIPTMERSNAGRYRCSY    91
```

FIG.10A

```
                *->GesvtLtCsvsgfgppgvsvtWyfkngk.lgpsllgysysrlesgek
                   G +vtL C++        ++  y k+g++ +       Y+r+e   +
mT268     128   GRDVTLKCQSP---YSFDEFVLY-KEGDtGP-------YKRPEKW-Y 162

                   anlsegrfsissltLtissvekeDsGtYtCvv<-*
                   +             ++i++v++  sGtY+C
mT268     163   RA-----------NFPIITVTAAHSGTYRCYS    183
```

FIG.10B

```
                10        20        30        40        50        60
inputs MSPSPTALFCLGLCLGRV-PAQSGPLPKPSLQALPSSLVPLEKPVTLRCQGPPGVDLYRLEKLSSSRYQD
       ::::: ::::::::: .: ::::::::::::: ::::::: ..:::::::::::::::::: . .:.:
       MSPASPTFFCIGLCVLQVIQTQSGPLPKPSLQAQPSSLVPLGQSVILRCQGPPDVDLYRLEKLKPEKYED
                10        20        30        40        50        60        70
           70        80        90       100       110       120       130
inputs QAVLFIPAMKRSLAGRYRCSYQNGSLWSLPSDQLELVATGVFAKPSLSAQPGPAVSSGGDVTLQCQTRYG
       :. :::::: :: ::::: :::::: :::::::::::::::::: :::.:.::. : :::::::. :.
       QDFLFIPTMERSNAGRYRCSYQNGSHWSLPSDQLELIATGVYAKPSLSAHPSSAVPQGRDVTLKCQSPYS
                80        90       100       110       120       130       140
      140       150       160       170       180       190       200
inputs FDQFALYKEGDPAPYKNPERWYRASFPIITVTAAMSGTYRCYSFSSRDPYLWSAPSDPLELVVTGTSVTP
       ::.:::::::: .::: ::::::::::::::::::::::::: .:::::::::::: ::::: :.::
       FDEFVLYKEGDTGPYKRPEKWYRANFPIITVTAAHSGTYRCYSFSSSSPYLWSAPSDPLVLVVTGLSATP
              150       160       170       180       190       200       210
      210       220       230       240       250       260       270
inputs SRLPTEPPSSVAEFSEATAELTVSFTNKVFTTETSRSITTSPKESDSPAGPARQYYTKGNLVRICLGAVI
       :.::: . .::: :   . :    :::. ::: . .::::    ..: : :.: :::::::::::::
       SQVPTEESFPVTESSRRPSILP---TNKISTTEKPMNITASPEGLSPPIGFAHQHYAKGNLVRICLGATI
              220       230       240       250       260       270

      280       290       300       310       320       330
inputs LIILAGFLAEDWHSRRKRLRHRGRAVQRPLPPLPPLPQTRKSHGGQDGGRQDVHSRGLCS
       .::: :.:::::::::.: :.:: :::.::::::::: :.
       IIILLGLLAEDWHSRKKCLQHRMRALQRPLPPLP-LA----------------------
       280       290       300       310
```

FIG.11